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RAW SEQUENCE LISTING   DATE: 07/10/2002
PATENT APPLICATION: US/10/037,591A   TIME: 13:05:38

Input Set : A:\37128C.txt
Output Set: N:\CRF3\07102002\J037591A.raw

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 4 <110> APPLICANT: Medlock, Eugene
 5       Yeh, Richard
 6       Silbiger, Scott M.
 7       Elliot, Gary S.
 8       Nguyen, Hung Q.
 9       Jing, Shuqian
11 <120> TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
13 <130> FILE REFERENCE: 01017/37128C
15 <140> CURRENT APPLICATION NUMBER: 10/037,591A
16 <141> CURRENT FILING DATE: 2002-06-24
18 <150> PRIOR APPLICATION NUMBER: 09/886,404
19 <151> PRIOR FILING DATE: 2001-06-21
21 <150> PRIOR APPLICATION NUMBER: 09/810,384
22 <151> PRIOR FILING DATE: 2001-03-16
24 <150> PRIOR APPLICATION NUMBER: 60/266,159
25 <151> PRIOR FILING DATE: 2001-02-02
27 <150> PRIOR APPLICATION NUMBER: 60/213,125
28 <151> PRIOR FILING DATE: 2000-06-22
30 <160> NUMBER OF SEQ ID NOS: 24
32 <170> SOFTWARE: PatentIn Ver. 2.0
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35 <211> LENGTH: 644
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (159)..(641)
43 <400> SEQUENCE: 1
44 ctcaagtcac tccctaaaaa gacagtggaa ataaatttga ataaacaaaa caggcttgct 60
46 gaaaataaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggcctgtcag 120
48 tcagtgcccc acttgtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176
49                                           Met Tyr Gln Val Val Ala
50                                            1               5
52 ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc   224
53 Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser
54             10              15              20
56 tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg   272
57 Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp
58             25              30              35
60 agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac   320
61 Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His
62         40              45              50
64 cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc   368
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65 Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala
66  55              60              65              70
68 atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc   416
69 Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro
70              75              80              85
72 cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta   464
73 Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu
74              90              95              100
76 cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac   512
77 Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr
78          105             110             115
80 cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc   560
81 His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
82      120             125             130
84 acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta   608
85 Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu
86 135             140             145             150
88 gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag                   644
89 Ala Cys Val Cys Val Arg Pro Arg Val Met Gly
90              155             160
93 <210> SEQ ID NO: 2
94 <211> LENGTH: 161
95 <212> TYPE: PRT
96 <213> ORGANISM: Homo sapiens
98 <400> SEQUENCE: 2
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100  1               5               10              15
102 Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
103              20              25              30
105 Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
106          35              40              45
108 Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
109      50              55              60
111 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
112  65              70              75              80
114 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
115              85              90              95
117 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
118              100             105             110
120 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro
121          115             120             125
123 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
124      130             135             140
127 Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
128 145             150             155             160
130 Gly
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 1013
135 <212> TYPE: DNA
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Input Set : A:\37128C.txt
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138 <220> FEATURE:
139 <221> NAME/KEY: CDS
140 <222> LOCATION: (1)..(507)
142 <400> SEQUENCE: 3
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144 Met Tyr Gln Ala Val Ala Phe Leu Ala Met Ile Val Gly Thr His Thr
145  1               5                  10                  15
147 gtc agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc    96
148 Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
149             20                  25                  30
151 ccc agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct   144
152 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
153          35                  40                  45
155 gca tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa   192
156 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
157      50                  55                  60
159 tcc tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct   240
160 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
161  65                  70                  75                  80
163 cct tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac   288
164 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
165                  85                  90                  95
167 ctg tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca   336
168 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
169             100                 105                 110
171 ggc tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac   384
172 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
173             115                 120                 125
175 cag acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat   432
176 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
177      130                 135                 140
179 cgc cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt   480
180 Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
181 145                 150                 155                 160
183 gtg tgt gtg cgg ccc cgg gtc atg gct tagtcatgct caccacctgc         527
184 Val Cys Val Arg Pro Arg Val Met Ala
185                  165
187 ctgaggctga tgcccggttg ggagagaggg ccaggtgtac aatcaccttg ccaatgcggg 587
189 ccgggttcaa gccctccaaa gccctacctg aagcagcagg ctcccgggac aagatggagg 647
191 acttggggag aaactctgac ttttgcactt tttggaagca cttttgggaa ggagcaggtt 707
193 ccgcttgtgc tgctagagga tgctgttgtg gcatttctac tcaggaacgg actccaaagg 767
195 cctgctgacc ctggaagcca tactcctggc tcctttcccc tgaatccccc aactcctggc 827
197 acaggcactt tctccacctc tccccctttg cctttgttg tgtttgtttg tgcatgccaa 887
199 ctctgcgtgc agccaggtgt aattgccttg aaggatggtt ctgaggtgaa agctgttatc 947
201 gaaagtgaag agatttatcc aaataaacat ctgtgtttaa aaaaaaaaaa aaaaaaaaaa 1007
203 aaaaaa                                                            1013
206 <210> SEQ ID NO: 4
207 <211> LENGTH: 169
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PATENT APPLICATION: US/10/037,591A   TIME: 13:05:38

Input Set : A:\37128C.txt
Output Set: N:\CRF3\07102002\J037591A.raw

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208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 4
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213  1               5                  10                  15
215 Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
216             20                  25                  30
218 Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
219             35                  40                  45
221 Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
222         50                  55                  60
224 Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
225  65                  70                  75                  80
227 Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
228             85                  90                  95
230 Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
231             100                 105                 110
233 Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
234         115                 120                 125
236 Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
237     130                 135                 140
239 Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
240 145                 150                 155                 160
242 Val Cys Val Arg Pro Arg Val Met Ala
243                 165
246 <210> SEQ ID NO: 5
247 <211> LENGTH: 155
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 5
252 Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu Ser
253  1               5                  10                  15
256 Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
257             20                  25                  30
259 Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
260             35                  40                  45
262 Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
263         50                  55                  60
265 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
266  65                  70                  75                  80
268 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
269             85                  90                  95
271 Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
272             100                 105                 110
274 Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
275         115                 120                 125
277 Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
278     130                 135                 140
280 Thr Cys Val Thr Pro Ile Val His His Val Ala
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PATENT APPLICATION: US/10/037,591A   TIME: 13:05:38

Input Set : A:\37128C.txt
Output Set: N:\CRF3\07102002\J037591A.raw

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281 145                   150                   155
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 117
286 <212> TYPE: PRT
287 <213> ORGANISM: Homo sapiens
289 <400> SEQUENCE: 6
290 Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu
291   1               5                  10                  15
293 Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys
294              20                  25                  30
296 Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
297          35                  40                  45
299 Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
300      50                  55                  60
302 Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
303   65                  70                  75                  80
305 Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
306                  85                  90                  95
308 Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Val Ala Gly
309              100                 105                 110
311 Cys Thr Cys Ile Phe
312          115
315 <210> SEQ ID NO: 7
316 <211> LENGTH: 117
317 <212> TYPE: PRT
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 7
321 Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu
322   1               5                  10                  15
325 Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys
326              20                  25                  30
328 Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
329          35                  40                  45
331 Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
332      50                  55                  60
334 Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
335   65                  70                  75                  80
337 Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
338                  85                  90                  95
340 Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly
341              100                 105                 110
343 Cys Thr Cys Ile Phe
344          115
347 <210> SEQ ID NO: 8
348 <211> LENGTH: 197
349 <212> TYPE: PRT
350 <213> ORGANISM: Homo sapiens
352 <400> SEQUENCE: 8
353 Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr Cys
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VERIFICATION SUMMARY   DATE: 07/10/2002
PATENT APPLICATION: US/10/037,591A   TIME: 13:05:39

Input Set : **A:\37128C.txt**
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